

## SEQUENCE LISTING

<110> Merck & Co., Inc.

<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE  
IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

<130> 21569Y PCT

<150> 60/489,840

<151> 2003-07-24

<150> 60/520,115

<151> 2003-11-14

<160> 107

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657n with amino terminus methionine

<400> 1

Met	Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr
1				5				10					15		
Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr
			20					25					30		
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala
		35					40					45			
Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala
	50					55					60				
Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn
65					70					75				80	
Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro
			85					90					95		
Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp
			100					105					110		
Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala
		115					120					125			
Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu
		130				135					140				
Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val
145					150					155				160	
Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr
			165						170				175		
Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys
			180					185					190		
Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys
		195					200					205			

```

Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala
 210                215                220
Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala
225                230                235                240
Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn
                245                250                255
Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys
                260                265                270
Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala
                275                280                285
Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp
                290                295                300
Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu
305                310                315                320
Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu
                325                330                335
Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp
                340                345                350
Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp
                355                360                365
Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys
                370                375                380
Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr
385                390                395                400
Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys
                405                410                415
Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala
                420                425                430
Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro
                435                440                445

```

<210> 2  
 <211> 645  
 <212> PRT  
 <213> S. aureus

```

<400> 2
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1                5                10                15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
                20                25                30
Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr
                35                40                45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
                50                55                60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                70                75                80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                90                95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
                100                105                110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
                115                120                125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
                130                135                140

```

Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly
145					150					155					160
Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val
				165						170					175
Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly
			180							185					190
Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro
		195					200					205			
Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg
	210					215					220				
Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr
225					230						235				240
His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe
				245					250						255
Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp
			260						265						270
Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu
		275					280						285		
Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu
	290					295					300				
Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala
305					310					315					320
Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln
			325						330						335
Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val
			340					345					350		
Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys
		355					360						365		
His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met
	370					375						380			
Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln
385					390					395					400
Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile
				405					410						415
Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys
			420					425					430		
Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile
		435					440						445		
Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys
	450					455					460				
Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr
465					470					475					480
Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln
				485					490						495
Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu
			500					505					510		
Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys
		515					520						525		
Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val
	530					535					540				
Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys
545					550					555					560
Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys
				565					570						575

Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn<sup>8</sup> Thr Asn Asp Gly  
                   580                  585                  590  
 His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys  
                   595                  600                  605  
 Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro  
           610                  615                  620  
 Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro  
 625                  630                  635                  640  
 Arg Lys Arg Lys Asn  
                   645

<210> 3

<211> 569

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH with amino terminus methionine

<400> 3

Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr  
 1                  5                  10                  15  
 Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr  
                   20                  25                  30  
 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala  
                   35                  40                  45  
 Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala  
                   50                  55                  60  
 Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn  
 65                  70                  75                  80  
 Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro  
                   85                  90                  95  
 Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp  
                   100                  105                  110  
 Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala  
                   115                  120                  125  
 Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu  
                   130                  135                  140  
 Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val  
 145                  150                  155                  160  
 Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr  
                   165                  170                  175  
 Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys  
                   180                  185                  190  
 Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys  
                   195                  200                  205  
 Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala  
                   210                  215                  220  
 Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala  
 225                  230                  235                  240  
 Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn  
                   245                  250                  255  
 Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys  
                   260                  265                  270

Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala  
 275 280 285  
 Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp  
 290 295 300  
 Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu  
 305 310 315 320  
 Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu  
 325 330 335  
 Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp  
 340 345 350  
 Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp  
 355 360 365  
 Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys  
 370 375 380  
 Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr  
 385 390 395 400  
 Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys  
 405 410 415  
 Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala  
 420 425 430  
 Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro  
 435 440 445  
 Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys  
 450 455 460  
 Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly  
 465 470 475 480  
 Lys Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser  
 485 490 495  
 Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala  
 500 505 510  
 Lys Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr  
 515 520 525  
 Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala  
 530 535 540  
 Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys  
 545 550 555 560  
 Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 4

&lt;211&gt; 570

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH with amino terminus methionine-glycine

&lt;400&gt; 4

Met Gly Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys  
 1 5 10 15  
 Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu  
 20 25 30  
 Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu  
 35 40 45

Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	50	55	60
Ala	Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	65	70	75
Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	85	90	95
Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	100	105	110
Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	115	120	125
Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	130	135	140
Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	145	150	155
Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	165	170	175
Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	180	185	190
Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	195	200	205
Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	210	215	220
Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	225	230	235
Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	245	250	255
Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	260	265	270
Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	275	280	285
Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	290	295	300
Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	305	310	315
Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	325	330	335
Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	340	345	350
Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	355	360	365
Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	370	375	380
Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	385	390	395
Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	405	410	415
Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	420	425	430
Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	435	440	445
Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	450	455	460
Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	465	470	475



Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu
				485					490					495	
Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val
			500					505					510		
Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln
		515					520					525			
Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys
	530					535					540				
Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn
545					550					555					560
Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser						
				565					570						

<210> 5

<211> 447

<212> PRT

<213> Artificial Sequence

**<220>**

<223> ORF0657nH with amino terminus methionine-glycine

<400> 5

Met 1	Gly	Ala	Glu	Glu 5	Thr	Gly	Gly	Thr	Asn 10	Thr	Glu	Ala	Gln	Pro 15	Lys
Thr	Glu	Ala	Val 20	Ala	Ser	Pro	Thr	Thr 25	Thr	Ser	Glu	Lys	Ala 30	Pro	Glu
Thr	Lys	Pro 35	Val	Ala	Asn	Ala	Val 40	Ser	Val	Ser	Asn	Lys 45	Glu	Val	Glu
Ala	Pro 50	Thr	Ser	Glu	Thr	Lys 55	Glu	Ala	Lys	Glu	Val 60	Lys	Glu	Val	Lys
Ala 65	Pro	Lys	Glu	Thr	Lys 70	Glu	Val	Lys	Pro	Ala 75	Ala	Lys	Ala	Thr	Asn 80
Asn	Thr	Tyr	Pro 85	Ile	Leu	Asn	Gln	Glu 90	Leu	Arg	Glu	Ala	Ile 95	Lys	Asn
Pro	Ala	Ile 100	Lys	Asp	Lys	Asp	His 105	Ser	Ala	Pro	Asn	Ser 110	Arg	Pro	Ile
Asp	Phe 115	Glu	Met	Lys	Lys	Lys	Asp 120	Gly	Thr	Gln	Gln	Phe 125	Tyr	His	Tyr
Ala 130	Ser	Ser	Val	Lys	Pro	Ala 135	Arg	Val	Ile	Phe	Thr 140	Asp	Ser	Lys	Pro
Glu 145	Ile	Glu	Leu	Gly 150	Leu	Gln	Ser	Gly	Gln	Phe 155	Trp	Arg	Lys	Phe	Glu 160
Val	Tyr	Glu	Gly 165	Asp	Lys	Lys	Leu	Pro	Ile 170	Lys	Leu	Val	Ser 175	Tyr	Asp
Thr	Val	Lys 180	Asp	Tyr	Ala	Tyr	Ile 185	Arg	Phe	Ser	Val	Ser 190	Asn	Gly	Thr
Lys	Ala 195	Val	Lys	Ile	Val	Ser	Ser 200	Thr	His	Phe	Asn	Asn 205	Lys	Glu	Glu
Lys 210	Tyr	Asp	Tyr	Thr	Leu	Met 215	Glu	Phe	Ala	Gln	Pro 220	Ile	Tyr	Asn	Ser
Ala 225	Asp	Lys	Phe	Lys 230	Thr	Glu	Glu	Asp	Tyr	Lys 235	Ala	Glu	Lys	Leu	Leu 240
Ala	Pro	Tyr	Lys 245	Lys	Ala	Lys	Thr	Leu	Glu 250	Arg	Gln	Val	Tyr 255	Glu	Leu

```

Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys
      260      265      270
Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser
      275      280      285
Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr
      290      295      300
Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn
305      310      315      320
Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met
      325      330      335
Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr
      340      345      350
Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys
      355      360      365
Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly
      370      375      380
Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp
385      390      395      400
Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr
      405      410      415
Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser
      420      425      430
Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro
      435      440      445

```

&lt;210&gt; 6

&lt;211&gt; 576

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 6

```

Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
      20      25      30
Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys
      35      40      45
Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys
      50      55      60
Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro
65      70      75      80
Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
      85      90      95
Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
      100      105      110
Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr
      115      120      125
Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
      130      135      140
Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
145      150      155      160

```



Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile  
 165 170 175  
 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe  
 180 185 190  
 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His  
 195 200 205  
 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala  
 210 215 220  
 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr  
 225 230 235 240  
 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu  
 245 250 255  
 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys  
 260 265 270  
 Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu  
 275 280 285  
 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro  
 290 295 300  
 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr  
 305 310 315 320  
 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Ala Phe Val Lys His  
 325 330 335  
 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu  
 340 345 350  
 Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg  
 355 360 365  
 Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile  
 370 375 380  
 Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val  
 385 390 395 400  
 His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 405 410 415  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys  
 420 425 430  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro  
 435 440 445  
 Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 450 455 460  
 Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn  
 465 470 475 480  
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro  
 485 490 495  
 Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val  
 500 505 510  
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr  
 515 520 525  
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp  
 530 535 540  
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His  
 545 550 555 560  
 Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570 575

&lt;210&gt; 7

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 7

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	1	5	10	15
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys	20	25	30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	35	40	45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	50	55	60	
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr	65	70	75	80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	85	90	95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	100	105	110	
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	115	120	125	
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	130	135	140	
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	145	150	155	160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	165	170	175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	180	185	190	
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	195	200	205	
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	210	215	220	
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	225	230	235	240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	245	250	255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	260	265	270	
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	275	280	285	
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	290	295	300	
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	305	310	315	320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	325	330	335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	340	345	350	
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	355	360	365	
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	370	375	380	

```

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                               390                               395                               400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                               405                               410                               415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                               420                               425                               430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                               435                               440                               445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                               450                               455                               460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                               470                               475                               480
Gly Val Thr Leu Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
                               485                               490                               495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                               500                               505                               510
Pro Thr Thr Gly Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                               515                               520                               525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
530                               535                               540
Ile Lys His Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                               550                               555                               560
Thr Gln Glu Asn Lys Ala Lys Ser
                               565

```

&lt;210&gt; 8

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 8

```

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1                               5                               10                               15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
                               20                               25                               30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
                               35                               40                               45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50                               55                               60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65                               70                               75                               80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
                               85                               90                               95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
                               100                               105                               110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
115                               120                               125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130                               135                               140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145                               150                               155                               160

```

Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 9

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 9

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	1	5	10	15
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys	20	25	30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	35	40	45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	50	55	60	
Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr	65	70	75	80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	85	90	95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	100	105	110	
Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	115	120	125	
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	130	135	140	
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	145	150	155	160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	165	170	175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	180	185	190	
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	195	200	205	
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	210	215	220	
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	225	230	235	240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	245	250	255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	260	265	270	
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	275	280	285	
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	290	295	300	
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	305	310	315	320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	325	330	335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	340	345	350	
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	355	360	365	
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	370	375	380	

```

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                      390                      395                      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                      405                      410                      415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                      420                      425                      430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                      435                      440                      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                      450                      455                      460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                      470                      475                      480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
                      485                      490                      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                      500                      505                      510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                      515                      520                      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
530                      535                      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                      550                      555                      560
Thr Gln Glu Asn Lys Ala Lys Ser
                      565

```

&lt;210&gt; 10

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 10

```

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1                      5                      10                      15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
                      20                      25                      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
                      35                      40                      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50                      55                      60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65                      70                      75                      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
                      85                      90                      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
                      100                      105                      110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
                      115                      120                      125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130                      135                      140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145                      150                      155                      160

```



Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Lys Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 11

&lt;211&gt; 565

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 11

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35					40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr
	50					55					60				
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile
65					70				75						80
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp
				85					90					95	
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys
			100					105					110		
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys
		115					120						125		
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly
	130					135					140				
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp
145					150					155					160
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr
				165					170					175	
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile
			180					185					190		
Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr
		195					200						205		
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys
	210					215					220				
Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys
225					230						235				240
Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp
				245					250					255	
Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Lys	Leu	Glu
			260					265						270	
Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe
		275					280						285		
Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr
	290					295					300				
Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp
305					310					315					320
Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys
				325					330					335	
Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met
			340					345					350		
Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn
		355					360					365			
Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp
	370					375						380			

Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr  
 500 505 510  
 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser  
 515 520 525  
 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn  
 530 535 540  
 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu  
 545 550 555 560  
 Asn Lys Ala Lys Ser  
 565

<210> 12  
 <211> 566  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 12  
 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160

Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro  
 500 505 510  
 Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly  
 515 520 525  
 Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys  
 530 535 540  
 Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln  
 545 550 555 560  
 Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 13

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 13

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
			35				40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
65					70					75					80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
				85				90					95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100					105					110		
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
			115				120						125		
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145					150					155					160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200						205		
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215						220			
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280						285		
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				

```

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                      390                      395                      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                      405                      410                      415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                      420                      425                      430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                      435                      440                      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                      450                      455                      460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                      470                      475                      480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Lys Val Glu Ser Ser
                      485                      490                      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                      500                      505                      510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                      515                      520                      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
.530                      535                      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                      550                      555                      560
Thr Gln Glu Asn Lys Ala Lys Ser
                      565

```

&lt;210&gt; 14

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 14

```

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1                      5                      10                      15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
                      20                      25                      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
                      35                      40                      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50                      55                      60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65                      70                      75                      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Glu
                      85                      90                      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
                      100                      105                      110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
                      115                      120                      125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130                      135                      140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145                      150                      155                      160

```



Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Ala	Ser	Tyr	Asp	Thr	Val	
				165					170					175		
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Ile	Ser	Asn	Gly	Thr	Lys	Ala	
			180					185					190			
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	
		195					200					205				
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	
	210				215				220							
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	
225					230				235						240	
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	
			245					250						255		
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	
		260					265						270			
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	
	275					280						285				
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	
	290					295					300					
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	
305					310				315						320	
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	
			325					330						335		
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	
		340					345						350			
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	
	355					360						365				
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	
	370					375					380					
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	
385					390				395						400	
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	
			405					410						415		
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	
		420						425					430			
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	
	435					440						445				
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	
	450					455					460					
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	
465					470				475						480	
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	
			485					490						495		
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Val	Lys	
		500						505					510			
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	
	515					520						525				
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	
	530					535					540					
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	
545					550				555						560	
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser									
				565												

&lt;210&gt; 15

&lt;211&gt; 564

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 15

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35					40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr
	50					55					60				
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile
65					70				75						80
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp
				85					90					95	
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys
			100					105					110		
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys
		115					120					125			
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly
	130					135					140				
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp
145					150					155					160
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr
				165					170					175	
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile
			180					185					190		
Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr
		195					200					205			
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys
	210					215					220				
Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys
225					230						235				240
Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp
				245					250					255	
Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Lys	Leu	Glu
			260					265						270	
Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe
		275					280						285		
Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr
	290					295					300				
Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp
305					310					315					320
Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys
				325					330					335	
Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met
			340					345					350		
Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn
		355					360					365			
Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp
	370					375					380				

Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Ala  
 500 505 510  
 Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser Ser  
 515 520 525  
 Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr  
 530 535 540  
 Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn  
 545 550 555 560  
 Lys Ala Lys Ser

<210> 16  
 <211> 565  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 16  
 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr  
 50 55 60  
 Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile  
 65 70 75 80  
 Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp  
 85 90 95  
 Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys  
 100 105 110  
 Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys  
 115 120 125  
 Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly  
 130 135 140  
 Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp  
 145 150 155 160

Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr  
 165 170 175  
 Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile  
 180 185 190  
 Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr  
 195 200 205  
 Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys  
 210 215 220  
 Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys  
 225 230 235 240  
 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp  
 245 250 255  
 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp  
 260 265 270  
 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe  
 275 280 285  
 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr  
 290 295 300  
 Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp  
 305 310 315 320  
 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys  
 325 330 335  
 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met  
 340 345 350  
 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn  
 355 360 365  
 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp  
 370 375 380  
 Ala Ile Val Arg Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr  
 500 505 510  
 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser  
 515 520 525  
 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn  
 530 535 540  
 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu  
 545 550 555 560  
 Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 17

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 17

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Leu	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Thr	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
			35				40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr
65					70					75					80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
				85				90					95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100					105					110		
Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
			115				120					125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145					150					155					160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215						220			
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280						285		
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Ile	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				

```

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                               390                               395                               400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                               405                               410                               415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                               420                               425                               430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                               435                               440                               445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                               450                               455                               460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                               470                               475                               480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
                               485                               490                               495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                               500                               505                               510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                               515                               520                               525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
530                               535                               540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                               550                               555                               560
Thr Gln Glu Asn Lys Ala Lys Ser
                               565

```

<210> 18  
 <211> 565  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

```

<400> 18
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1                               5                               10                               15
Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
                               20                               25                               30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
35                               40                               45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr
50                               55                               60
Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile
65                               70                               75                               80
Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp
85                               90                               95
Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys
100                               105                               110
Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys
115                               120                               125
Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly
130                               135                               140
Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp
145                               150                               155                               160

```



Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr  
 165 170 175  
 Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile  
 180 185 190  
 Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr  
 195 200 205  
 Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys  
 210 215 220  
 Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys  
 225 230 235 240  
 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp  
 245 250 255  
 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp  
 260 265 270  
 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe  
 275 280 285  
 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr  
 290 295 300  
 Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp  
 305 310 315 320  
 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys  
 325 330 335  
 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met  
 340 345 350  
 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn  
 355 360 365  
 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp  
 370 375 380  
 Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Pro Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr  
 500 505 510  
 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser  
 515 520 525  
 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn  
 530 535 540  
 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu  
 545 550 555 560  
 Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 19

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 19

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	1	5	10	15
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys	20	25	30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	35	40	45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	50	55	60	
Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro	Ala	Thr	Lys	Ala	Asp	Asn	Asn	Thr	65	70	75	80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	85	90	95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	100	105	110	
Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	115	120	125	
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	130	135	140	
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	145	150	155	160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	165	170	175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	180	185	190	
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	195	200	205	
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	210	215	220	
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	225	230	235	240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	245	250	255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	260	265	270	
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	275	280	285	
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	290	295	300	
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	305	310	315	320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	325	330	335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	340	345	350	
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	355	360	365	
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	370	375	380	

```

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                               390                               395                               400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                               405                               410                               415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                               420                               425                               430
Arg Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                               435                               440                               445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                               450                               455                               460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                               470                               475                               480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
                               485                               490                               495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                               500                               505                               510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                               515                               520                               525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
530                               535                               540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                               550                               555                               560
Thr Gln Glu Asn Lys Ala Lys Ser
                               565

```

<210> 20  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

```

<400> 20
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1                               5                               10                               15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
                               20                               25                               30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
35                               40                               45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50                               55                               60
Lys Glu Thr Lys Ala Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr
65                               70                               75                               80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
85                               90                               95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
100                               105                               110
Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser
115                               120                               125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130                               135                               140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145                               150                               155                               160

```

Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 21

&lt;211&gt; 576

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 21

Ala	Glu	Glu	Thr	Gly	Val	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala
			20					25					30		
Lys	Pro	Val	Ala	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys
		35					40					45			
Glu	Val	Val	Ala	Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys
	50					55					60				
Ala	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro
65					70					75					80
Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu
			85						90				95		
Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala
			100					105					110		
Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr
		115					120					125			
Gln	Gln	Phe	Tyr	His	Tyr	Ala	Gly	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile
	130					135					140				
Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln
145					150					155					160
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile
			165						170					175	
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe
			180					185					190		
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His
		195					200					205			
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala
	210					215					220				
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr
225					230					235					240
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu
			245						250					255	
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys
			260					265					270		
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu
		275					280					285			
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro
	290					295					300				
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr
305					310					315					320
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His
			325						330					335	
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu
			340					345					350		
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
		355					360					365			
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile
	370					375					380				

Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val  
 385 390 395 400  
 His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 405 410 415  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys  
 420 425 430  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro  
 435 440 445  
 Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 450 455 460  
 Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Gly Val Glu Lys Glu Asn  
 465 470 475 480  
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro  
 485 490 495  
 Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val  
 500 505 510  
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr  
 515 520 525  
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp  
 530 535 540  
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His  
 545 550 555 560  
 Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570 575

&lt;210&gt; 22

&lt;211&gt; 576

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 22

Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala  
 20 25 30  
 Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys  
 35 40 45  
 Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys  
 50 55 60  
 Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro  
 65 70 75 80  
 Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu  
 85 90 95  
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala  
 100 105 110  
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr  
 115 120 125  
 Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile  
 130 135 140  
 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln  
 145 150 155 160



Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile		
				165					170					175			
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe		
			180					185					190				
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His		
		195					200					205					
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala		
	210					215					220						
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr		
225					230				235					240			
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu		
				245					250					255			
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys		
			260					265					270				
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu		
		275					280					285					
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro		
	290					295					300						
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr		
305					310					315					320		
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His		
				325					330					335			
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu		
			340					345					350				
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg		
		355					360					365					
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile		
	370					375					380						
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val		
385					390					395				400			
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val		
				405					410					415			
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Ala	Asp	Lys	Thr	Asn	Lys	Lys		
			420				425						430				
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Thr	Thr	Pro	Ala	Met	Pro		
		435					440					445					
Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp		
	450					455						460					
Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn		
465					470					475				480			
Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Met	Pro	Val	Thr	Lys	Pro		
				485					490					495			
Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val		
			500					505					510				
Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr		
		515					520					525					
Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp		
	530					535					540						
Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His		
545					550					555				560			
Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser		
				565					570					575			

&lt;210&gt; 23

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 23

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	1	5	10	15
Ala	Val	Ala	Ser	Pro	Ser	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys	20	25	30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	35	40	45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	50	55	60	
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Thr	Lys	Ala	Asp	Asn	Asn	Thr	65	70	75	80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	85	90	95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	100	105	110	
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	115	120	125	
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	130	135	140	
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	145	150	155	160
Glu	Gly	Asn	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	165	170	175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	180	185	190	
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	195	200	205	
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Gly	210	215	220	
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ser	Pro	225	230	235	240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	245	250	255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	260	265	270	
Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	275	280	285	
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	290	295	300	
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	305	310	315	320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	325	330	335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Asn	Asp	Asp	Tyr	Trp	Lys		340	345	350	
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	355	360	365	
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	370	375	380	

```

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                               390                               395                               400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                               405                               410                               415
Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                               420                               425                               430
Lys Glu Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Pro Pro Val
                               435                               440                               445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                               450                               455                               460
Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                               470                               475                               480
Asp Lys Thr Pro Thr Thr Lys Pro Ala Lys Ala Glu Val Glu Ser Ser
                               485                               490                               495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                               500                               505                               510
Pro Thr Thr Ala Ser Ser Glu Thr Thr Ile Asp Val Val Gln Thr Ser
                               515                               520                               525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
530                               535                               540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Glu Asn Asn Lys Asn
545                               550                               555                               560
Thr Gln Glu Asn Lys Ala Lys Ser
                               565

```

<210> 24  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

```

<400> 24
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1                               5                               10                               15
Ala Val Ala Ser Pro Ser Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
                               20                               25                               30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
                               35                               40                               45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50                               55                               60
Lys Glu Thr Lys Glu Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr
65                               70                               75                               80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
                               85                               90                               95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
                               100                              105                              110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
                               115                              120                              125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130                              135                              140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145                              150                              155                              160

```

Glu	Gly	Asn	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ser	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
				405					410					415	
Asn	Ala	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Thr	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val
		435					440					445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455					460				
Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465					470					475					480
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser
				485					490					495	
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys
			500					505					510		
Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr	Thr	Ile	Asp	Val	Val	Gln	Thr	Ser
		515					520						525		
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn
	530					535					540				
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Glu	Asn	Asn	Lys	Asn
545					550					555					560
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser								
				565											

&lt;210&gt; 25

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 25

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Ile	Thr	Glu	Thr	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Ala	Ala	Pro
		35				40					45				
Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Asn	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ser	Asp	Asn	Asn	Thr
65				70						75					80
Tyr	Pro	Ile	Leu	Asn	Glu	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
			85					90					95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
		100					105						110		
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
		115				120						125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135				140					
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145				150						155					160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
			165					170					175		
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
		180				185							190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
	195					200						205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210				215						220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225				230						235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
			245					250					255		
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
		260				265							270		
Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
	275					280						285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290			295						300					
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305				310					315						320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
			325					330					335		
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
		340				345						350			
Asp	Phe	Met	Val	Glu	Gly	Glu	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
	355					360					365				
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370				375						380				

```

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                               390                               395                               400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                               405                               410                               415
Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                               420                               425                               430
Lys Glu Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Ala Pro Val
                               435                               440                               445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                               450                               455                               460
Ser Pro Ser Val Glu Lys Glu Ile Asp Ala Ser Ser Glu Ser Gly Lys
465                               470                               475                               480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
                               485                               490                               495
Ser Thr Thr Pro Thr Lys Val Val Ser Ala Thr Gln Asn Val Ala Lys
                               500                               505                               510
Pro Thr Ser Ala Ser Ser Glu Thr Thr Lys Gly Val Val Gln Thr Ser
                               515                               520                               525
Ala Gly Ser Ser Glu Ala Lys Asp Asn Ala Pro Leu Gln Lys Ala Asn
530                               535                               540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                               550                               555                               560
Thr Gln Glu Asn Lys Ala Lys Ser
                               565

```

<210> 26  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

```

<400> 26
Ala Glu Glu Thr Gly Gly Thr Ile Thr Glu Thr Gln Pro Lys Thr Glu
1                               5                               10                               15
Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
                               20                               25                               30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala Pro
                               35                               40                               45
Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50                               55                               60
Asn Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ser Asp Asn Asn Thr
65                               70                               75                               80
Tyr Pro Ile Leu Asn Glu Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
                               85                               90                               95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
                               100                              105                              110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
                               115                              120                              125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130                              135                              140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145                              150                              155                              160

```



Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Glu Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Ala Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Ser Pro Ser Val Glu Lys Glu Ile Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Ala Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Ser Ala Ser Ser Glu Thr Thr Lys Gly Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Asn Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 27

&lt;211&gt; 570

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 27

Met	Gly	Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	1	5	10	15
Thr	Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	20	25	30	
Thr	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	35	40	45	
Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	50	55	60	
Ala	Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	65	70	75	80
Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	85	90	95	
Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	100	105	110	
Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	115	120	125	
Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	130	135	140	
Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	145	150	155	160
Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	165	170	175	
Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	180	185	190	
Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	195	200	205	
Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	210	215	220	
Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	225	230	235	240
Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	245	250	255	
Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	260	265	270	
Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	275	280	285	
Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	290	295	300	
Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	305	310	315	320
Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	325	330	335	
Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	340	345	350	
Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	355	360	365	
Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	370	375	380	

```

Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp
385                               390                               395                               400
Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr
                               405                               410                               415
Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser
                               420                               425                               430
Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser
                               435                               440                               445
Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn
                               450                               455                               460
Lys Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser
465                               470                               475                               480
Gly Lys Gly Val Thr Leu Ala Thr Lys Pro Thr Lys Gly Glu Val Glu
                               485                               490                               495
Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val
                               500                               505                               510
Ala Lys Pro Thr Thr Gly Ser Ser Lys Thr Thr Lys Asp Val Val Gln
                               515                               520                               525
Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys
530                               535                               540
Ala Asn Ile Lys His Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn
545                               550                               555                               560
Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
                               565                               570

```

&lt;210&gt; 28

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> SEQ ID NO: 2 modified to contain a glycine after  
the amino terminus methionine and a carboxyl  
His-Tag

&lt;400&gt; 28

```

Met Gly Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg
1                               5                               10                               15
Lys Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu
                               20                               25                               30
Leu Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly
35                               40                               45
Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr
50                               55                               60
Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val
65                               70                               75                               80
Ser Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu
85                               90                               95
Ala Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val
100                               105                               110
Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln
115                               120                               125
Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His
130                               135                               140

```

Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp
145					150					155					160
Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg
				165					170						175
Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser
			180					185							190
Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu
		195					200					205			
Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile
	210					215					220				
Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser
225					230					235					240
Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu
			245						250						255
Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu
			260					265							270
Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr
		275					280					285			
Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro
	290					295					300				
Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys
305					310					315					320
Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val
			325						330						335
Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val
			340					345							
Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val
		355					360					365			
Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val
	370					375					380				
Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly
385					390					395					400
Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr
			405						410						415
Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val
			420					425					430		
Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg
		435					440					445			
Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn
	450					455					460				
Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala
465					470					475					480
Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys
			485						490						495
Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys
			500					505							
Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr
		515					520					525			
Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys
	530					535					540				
Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser
545					550					555					560
Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala
			565						570						575

Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp  
 580 585 590  
 Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala  
 595 600 605  
 Lys Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu  
 610 615 620  
 Pro Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu  
 625 630 635 640  
 Pro Arg Lys Arg Lys Asn Leu Glu His His His His His His  
 645 650

<210> 29  
 <211> 1962  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Full length ORF0657n + Carboxyl His-Tag

<400> 29  
 atgaacaaac agcaaaaaga atttaaataca ttttattcaa ttagaaagtc atcactaggc 60  
 gttgcatctg tagcaattag tacactttta ttattaatgt caaatggcga agcacaagca 120  
 gcagctgaag aaacaggtgg tacaaataca gaagcacaac caaaaactga agcagttgca 180  
 agtccaacaa caacatctga aaaagctcca gaaactaac cagtagctaa tgctgtctca 240  
 gtatctaata aagaagttga ggcccctact tctgaaacaa aagaagctaa agaagttaaa 300  
 gaagttaaag cccctaagga acaaaaagaa gttaaaccag cagcaaaagc cactaacaat 360  
 acatatccta ttttgaatca ggaacttaga gaagcgatta aaaaccctgc aataaaaagac 420  
 aaagatcata gcgcacacaaa ctctcgtcca attgattttg aaatgaaaaa gaaagatgga 480  
 actcaacagt tttatcatta tgcaagttct gttaaaccctg ctagagttat tttcactgat 540  
 tcaaaaccag aaattgaatt aggattacaa tcaggtcaat tttggagaaa atttgaagtt 600  
 tatgaaggtg acaaaaagtt gccaatataa ttagtatcat acgatactgt taaagattat 660  
 gcttacattc gcttctctgt atcaaacgga acaaaagctg ttaaaattgt tagttcaaca 720  
 cacttcaata acaaagaaga aaaatacgat tacacattaa tggaattcgc acaaccaatt 780  
 tataacagtg cagataaatt caaaactgaa gaagattata aagctgaaaa attattagcg 840  
 ccatataaaa aagcgaaaac actagaaaga caagtttatg aattaaataa aattcaagat 900  
 aaacttcctg aaaaattaaa ggctgagtag aagaagaaat tagaggatac aaagaaagct 960  
 ttagatgagc aagtgaatc agctattact gaattccaaa atgtacaacc aacaaatgaa 1020  
 aaaatgactg atttacaaga taaaaaatat gttgtttatg aaagtgttga gaataacgaa 1080  
 tctatgatgg atacttttgt taaacaccct attaaaacag gtatgcttaa cggcaaaaaa 1140  
 tatatggtca tggaaactac taatgacgat tactggaaag atttcatggt tgaaggtcaa 1200  
 cgtgttagaa ctataagcaa agatgctaaa aataatacta gaacaattat tttcccatat 1260  
 gttgaaggta aaactctata tgatgctatc gttaaagttc acgtaaaaac gattgattat 1320  
 gatggacaat accatgtcag aatcgttgat aaagaagcat ttacaaaagc caataccgat 1380  
 aaatctaaca aaaaagaaca acaagataac tcagctaaga aggaagctac tccagctacg 1440  
 cctagcaaac caacaccatc acctgttgaa aaagaatcac aaaaacaaga cagccaaaaa 1500  
 gatgacaata aacaattacc aagtgttgaa aaagaaaatg acgcatctag tgagtcaggt 1560  
 aaagacaaaa cgcttgctac aaaaccaact aaaggtgaag tagaatcaag tagtacaact 1620  
 ccaactaagg tagtatctac gactcaaaat gttgcaaaac caacaactgc ttcataaaaa 1680  
 acaacaaaag atgttggttca aacttcagca ggttctagcg aagcaaaaga tagtgctcca 1740  
 ttacaaaaag caaacattaa aaacacaaat gatggacaca ctcaaagcca aaacaataaa 1800  
 aatacacaag aaaataaagc aaaatcatta ccacaaactg gtgaagaatc aaataaagat 1860  
 atgacattac cattaatggc attattagct ttaagtagca tcgttgcatc cgtattacct 1920  
 agaaaacgta aaaacctcga gcaccaccac caccaccact ga 1962

<210> 30



&lt;211&gt; 1737

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH + Carboxyl His-Tag

&lt;400&gt; 30

```

atgaacgctg aagaaacagg tggtaacaaat acagaagcac aaccaaaaac tgaagcagtt 60
gcaagtccaa caacaacatc tgaaaaagct ccagaaacta aaccagtagc taatgctgtc 120
tcagtatcta ataaagaagt tgaggcccct acttctgaaa caaaagaagc taaagaagtt 180
aaagaagtta aagcccctaa ggaaacaaaa gaagttaaac cagcagcaaa agccactaac 240
aatacatatc ctatttttgaa tcaggaactt agagaagcga ttaaaaaccc tgcaataaaa 300
gacaaagatc atagcgcacc aaactctcgt ccaattgatt ttgaaatgaa aaagaaagat 360
ggaactcaac agtttttatca ttatgcaagt tctgttaaac ctgctagagt tatttttact 420
gattcaaaac cagaaattga attaggatta caatcaggtc aatttttgag aaaatttgaa 480
gtttatgaag gtgacaaaaa gttgccaaat aaattagtat catacgatac tgttaaagat 540
tatgcttaca ttcgcttctc tgtatcaaac ggaacaaaag ctgttaaaat tgttagttca 600
acacacttca ataacaaaga agaaaaatac gattacacat taatggaatt cgcacaacca 660
atttataaca gtgcagataa attcaaaaact gaagaagatt ataaagctga aaaattatta 720
gcgccatata aaaaagcgaa aacactagaa agacaagttt atgaattaaa taaaattcaa 780
gataaacttc ctgaaaaaatt aaaggctgag tacaagaaga aattagagga tacaagaaa 840
gcttttagatg agcaagtga atcagctatt actgaattcc aaaatgtaca accaacaat 900
gaaaaaatga ctgatttaca agatacaaaa tatgtttgtt atgaaagtgt tgagaataac 960
gaatctatga tggatacttt tgttaaacac cctattaaaa caggtatgct taacggcaaa 1020
aaatatatgg tcatggaaac tactaatgac gattactgga aagatttcat ggttgaaggt 1080
caacgtgtta gaactataag caaagatgct aaaaataata ctagaacaat tattttccca 1140
tatgttgaag gtaaaactct atatgatgct atcgttaaag ttcacgtaaa aacgattgat 1200
tatgatggac aataccatgt cagaatcgtt gataaagaag catttacaaa agccaatacc 1260
gataaatcta acaaaaaaga acaacaagat aactcagcta agaaggaagc tactccagct 1320
acgcctagca aaccaacacc atcacctgtt gaaaaagaat cacaaaaaca agacagccaa 1380
aaagatgaca ataaacaatt accaagtgtt gaaaaagaaa atgacgcac tagtgagtca 1440
ggtaaagaca aaacgcctgc tacaaaacca actaaagggtg aagtagaatc aagtagtaca 1500
actccaacta aggtagtatc tacgactcaa aatgttgcaa aaccaacaac tgcttcatca 1560
aaaacaacaa aagatgttgt tcaaacttca gcaggttcta gcgaagcaaa agatagtgtc 1620
ccattacaaa aagcaaacat taaaacaca aatgatggac acactcaaag ccaaaacaat 1680
aaaaatacac aagaaaataa agcaaaatca ctcgagcacc accaccacca ccactga 1737

```

&lt;210&gt; 31

&lt;211&gt; 1941

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 28 without a carboxyl His-Tag  
and is codon optimized for yeast expression

&lt;400&gt; 31

```

atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
ggtgttgctt ctgtcgctat ctccaccttg ttgttggtga tgtctaacgg tgaagctcaa 120
gctgctgctg aagaaactgg tggtaaccaac actgaagctc aaccaagac cgaagctgtc 180
gcttcccaa ccactacctc tgaaaaggct ccagaaacta agccagttgc taacgctgtc 240
tccgtttcta acaaggaagt cgaagctcca acctccgaaa ctaaggaagc taaggaagtt 300
aaggaagtca aggctccaaa ggaaactaag gaagtcaagc cagctgctaa ggctaccaac 360
aacacttacc caattttgaa ccaagaattg agagaagcta ttaagaaccc agctatcaag 420

```



```

gacaaggacc actccgctcc aaactctaga ccaatcgact tcgaaatgaa gaagaaggac 480
ggtacccaac aattctacca ctacgcgtcc tctgtcaagc cagctagagt tattttcacc 540
gactctaagc cagaaatcga attgggtttg caatccggtc aattctggag aaagttcgaa 600
gtctacgaag gtgacaagaa gttgccaatt aagttggttt cctacgacac cgtcaaggac 660
tacgcttaca tcagattctc cgtttctaac ggtactaagg ctgtcaagat tgtctcttcc 720
acccacttca acaacaagga agaaaagtac gactacactt tgatggaatt cgctcaacca 780
atttacaact ctgctgacaa gttcaagacc gaagaagact acaaggctga aaagttgttg 840
gtcccataca agaaggctaa gactttggaa agacaagttt acgaattgaa caagatccaa 900
gacaagttgc cagaaaagtt gaaggctgaa tacaagaaga agttggaaga caccaagaag 960
gctttggacg aacaagtcaa gtccgctatc accgaattcc aaaacgttca accaactaac 1020
gaaaagatga ctgacttgca agacactaag tacgtcgtct acgaatccgt cgaaaacaac 1080
gaatccatga tggacacctt cgtaagcac ccaattaaga ctgggtatgtt gaacggtaag 1140
aagtacatgg tcatggaaac cactaacgac gactactgga aggacttcat ggttgaagg 1200
caaagagtca gaaccatctc caaggacgct aagaacaaca ctagaacat tatcttccca 1260
tacgttgaag gtaagacttt gtacgacgct atcgtcaagg ttcacgtcaa gactattgac 1320
tacgacggtc aataccacgt tagaattgtt gacaaggaag ctttcaccaa ggctaacacc 1380
gacaagtcca acaagaagga acaacaagac aactctgcta agaaggaagc taccacagct 1440
accccatcta agccaacccc atctccagtt gaaaaggaat ctcaaaagca agactcccaa 1500
aaggacgaca acaagcaatt gccatccgtc gaaaaggaaa acgacgcgtc ttctgaatcc 1560
ggtaaggaca agactccagc taccaagcca actaagggtg aagttgaatc ttctctact 1620
actccaacca aggttgtctc cactacccaa aacgtcgtc agccaactac cgcttcttcc 1680
aagactacca aggacgttgt ccaaacttct gctggttcct ctgaagctaa ggactctgct 1740
ccattgcaaa aggctaacat caagaacacc aacgacggtc acaccaatc ccaaaacaac 1800
aagaacactc aagaaaacaa ggctaagtct ttgccacaaa ccggtgaaga atccaacaag 1860
gacatgacct tgccattgat ggctttgttg gctttgtctt ccatcgttgc tttcgtcttg 1920
ccaagaaaga gaaagaacta a

```

&lt;210&gt; 32

&lt;211&gt; 1710

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 3 and is codon optimized for yeast expression

&lt;400&gt; 32

```

atggctgaag aaactgggtg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtgaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080

```

```

agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

<210> 33

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 1 and is codon optimized for yeast expression

<400> 33

```

atgggtgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataag ttggtttctt acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccata a 1341

```

<210> 34

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus methionine and is codon optimized for yeast expression

&lt;400&gt; 34

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttag tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattggtgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctgtctc tgaatccggt 1440
aaggggtgtca ctttgggtac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

&lt;210&gt; 35

&lt;211&gt; 1710

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 7 containing an amino terminus methionine and is codon optimized for yeast expression

&lt;400&gt; 35

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttag tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720

```

```

ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aagggcgtca ctttggctac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

&lt;210&gt; 36

&lt;211&gt; 1710

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 7 containing an amino terminus  
methionine and is codon optimized for yeast  
expression

&lt;400&gt; 36

```

atggctgaag aaactgggtg taccacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctaccttga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccacaac 240
acttaccxaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aaggggtgtta ctttggctac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560

```



actaccaagg acgttgtcca aacttctgct gggttcctctg aagctaagga ctctgctcca 1620  
 ttgcaaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggc taagtcttaa 1710

<210> 37

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus  
 methionine and is codon optimized for yeast  
 expression

<400> 37

atggctgaag aaactgggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60  
 tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120  
 gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180  
 gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360  
 acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480  
 tacgaagggtg acaagaagtt gccaatataag ttggtttctt acgacaccgt caaggactac 540  
 gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720  
 ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acaccttcgt taagcaccca attagactg gtatgttgaa cggtaagaag 1020  
 tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080  
 agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140  
 gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200  
 gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac ccagctacc 1320  
 ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380  
 gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440  
 aagggcggtta ctttgggtac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500  
 ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560  
 actaccaagg acgttgtcca aacttctgct gggttcctctg aagctaagga ctctgctcca 1620  
 ttgcaaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680  
 aacactcaag aaaacaaggc taagtcttaa 1710

<210> 38

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus  
 methionine and is codon optimized for yeast  
 expression

&lt;400&gt; 38

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt ggggttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattggtgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aagggtgtca ctttagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

&lt;210&gt; 39

&lt;211&gt; 1710

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 7 containing an amino terminus  
methionine and is codon optimized for yeast  
expression

&lt;400&gt; 39

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt ggggttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780

```



```

aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aaggggtgtca ctttggctac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ctcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

&lt;210&gt; 40

&lt;211&gt; 1710

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 7 containing an amino terminus  
methionine and is codon optimized for yeast  
expression

&lt;400&gt; 40

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aaggggtgtta ctttagctac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620

```

ttgcaaaaagg ctaacatcaa gcacaccaac gacgggtcaca cccaatccca aaacaacaag 1680  
aacactcaag aaaacaaggc taagtcttaa 1710

<210> 41

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus  
methionine and is codon optimized for yeast  
expression

<400> 41

```
atggctgaag aaactgggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttcttaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat ctcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgtagg aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aaggggtgta ctttggtctac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ctcttccaag 1560
actaccaagg acgttggtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaaagg ctaacatcaa gcacaccaac gacgggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710
```

<210> 42

<211> 481

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nI+

<400> 42

```
Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr
  1                      5                      10                      15
```

Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr
		20						25					30		
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala
		35					40					45			
Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala
	50					55					60				
Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn
65					70					75				80	
Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro
			85						90					95	
Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp
			100					105					110		
Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala
		115					120					125			
Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu
	130					135					140				
Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val
145					150					155				160	
Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr
			165						170					175	
Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys
			180					185					190		
Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys
		195					200					205			
Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala
	210					215					220				
Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala
225					230					235				240	
Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn
				245					250					255	
Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys
			260					265					270		
Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala
		275					280					285			
Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp
	290					295					300				
Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu
305					310					315				320	
Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu
			325					330						335	
Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp
			340					345					350		
Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp
		355					360					365			
Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys
	370					375					380				
Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr
385					390					395				400	
Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys
				405					410					415	
Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala
			420					425					430		
Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro
		435					440						445		

Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys  
 450 455 460  
 Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly  
 465 470 475 480  
 Lys

<210> 43  
 <211> 1452  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes SEQ ID NO: 42 and is codon optimized for  
 yeast expression

<400> 43  
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60  
 tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120  
 gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180  
 gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360  
 acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480  
 tacgaagggtg acaagaagtt gccaatattag ttggtttcct acgacaccgt caaggactac 540  
 gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720  
 ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgctcg aaacaacgaa 960  
 tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020  
 tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080  
 agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140  
 gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200  
 gacggtcaat accacgtag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320  
 ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380  
 gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440  
 aagtaaggat cc 1452

<210> 44  
 <211> 605  
 <212> PRT  
 <213> ORF0657nG

<400> 44  
 Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr  
 1 5 10 15  
 Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr  
 20 25 30  
 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala  
 35 40 45

- 55 -



Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	
				485					490					495		
Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	
			500					505					510			
Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	
		515					520					525				
Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	
	530					535					540					
Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	
545					550					555					560	
Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser	Leu	Pro	Gln	Thr	Gly	Glu	Glu	
				565					570					575		
Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro	Leu	Met	Ala	Leu	Leu	Ala	Leu	Ser	
			580					585					590			
Ser	Ile	Val	Ala	Phe	Val	Leu	Pro	Arg	Lys	Arg	Lys	Asn				
		595					600					605				

&lt;210&gt; 45

&lt;211&gt; 1818

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 44 containing an amino terminus methionine and is codon optimized for yeast expression

&lt;400&gt; 45

atggctgaag	aaactggtgg	taccaacact	gaagctcaac	caaagaccga	agctgtcgct	60
tccccaacca	ctacctctga	aaaggctcca	gaaactaagc	cagttgctaa	cgctgtctcc	120
gttttctaaca	aggaagtcga	agctccaacc	tccgaaacta	aggaagctaa	ggaagttaag	180
gaagtcaagg	ctccaaagga	aactaaggaa	gtcaagccag	ctgctaaggc	taccaacaac	240
acttacccaa	ttttgaacca	agaattgaga	gaagctatta	agaaccacgc	tatcaaggac	300
aaggaccact	ccgctccaaa	ctctagacca	atcgacttcg	aaatgaagaa	gaaggacggt	360
acccaacaat	tctaccacta	cgcgtcctct	gtcaagccag	ctagagttaa	tttcaccgac	420
tctaagccag	aaatcgaatt	gggtttgcaa	tccggtcaat	tctggagaaa	gttcgaagtc	480
tacgaaggtg	acaagaagtt	gccaattaag	ttggtttctt	acgacaccgt	caaggactac	540
gcttacatca	gattctccgt	ttctaaccgt	actaaggctg	tcaagattgt	ctcttccacc	600
cacttcaaca	acaaggaaga	aaagtacgac	tacactttga	tggaaattcg	tcaaccaatt	660
tacaactctg	ctgacaagtt	caagaccgaa	gaagactaca	aggctgaaaa	gttggttggt	720
ccatacaaga	aggctaagac	tttggaagaa	caagtttacg	aattgaacaa	gatccaagac	780
aagttgccag	aaaagttgaa	ggctgaatac	aagaagaagt	tggaaagacac	caagaaggct	840
ttggacgaac	aagtcaagtc	cgctatcacc	gaattccaaa	acgttcaacc	aactaacgaa	900
aagatgactg	acttgcaaga	cactaagtac	gtcgtctacg	aatccgtcga	aaacaacgaa	960
tccatgatgg	acaccttcgt	taagcaccca	attaagactg	gtatgttgaa	cggtaagaag	1020
tacatggtca	tggaaaccac	taacgacgac	tactggaagg	acttcatggt	tgaaggtaa	1080
agagtcagaa	ccatctccaa	ggacgctaag	aacaacacta	gaaccattat	cttcccatac	1140
gttgaaggta	agactttgta	cgacgctatc	gtcaaggttc	acgtcaagac	tattgactac	1200
gacggtcaat	accacgtag	aattgttgac	aaggaagctt	tcaccaaggc	taacaccgac	1260
aagtccaaca	agaaggaaca	acaagacaac	tctgctaaga	aggaagctac	cccagctacc	1320
ccatctaagc	caaccccatc	tccagttgaa	aaggaatctc	aaaagcaaga	ctcccaaaaag	1380
gacgacaaca	agcaattgcc	atccgtcgaa	aaggaaaacg	acgcgtcttc	tgaatccggt	1440
aaggacaaga	ctccagctac	caagccaact	aagggtgaag	ttgaatcttc	ctctactact	1500
ccaaccaagg	ttgtctccac	tacccaaaac	gtcgctaagc	caactaccgc	ttcttccaag	1560
actaccaagg	acgttggtcca	aacttctgct	ggttcctctg	aagctaagga	ctctgctcca	1620



```

ttgcaaaagg ctaacatcaa gaacaccaac gacgggcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1740
atgaccttgc cattgatggc tttgttggtt ttgtcttcca tcgttgcttt cgtcttgcca 1800
agaaagagaa agaactaa                                     1818

```

<210> 46

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 17 containing an amino terminus methionine and is codon optimized for yeast expression

<400> 46

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttgggt 60
tccccaacca ctaccactga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataa ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttgggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgtagg aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacgggcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa                                     1710

```

<210> 47

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes the SEQ ID NO: 17 I+ region, is codon optimized for yeast expression, and encodes a methionine initiation codon

&lt;400&gt; 47

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 60
tccccaacca ctaccactga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttaa tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataa ttggtttctt acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggtggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccga attagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtaa 1080
agagtcagaa ccactctcaa ggacgctaag aacaacacta gaaccattat cttcccatc 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgtagg aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcga aaggaaaacg acgctcttc tgaatccggt 1440
aagtaa 1446

```

&lt;210&gt; 48

&lt;211&gt; 1341

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes the SEQ ID NO: 17 I region, is codon optimized for yeast expression, and encodes a methionine initiation codon

&lt;400&gt; 48

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 60
tccccaacca ctaccactga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttaa tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataa ttggtttctt acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggtggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960

```

```

tccatgatgg acaccttcgt taagcaccca attaagactg gtatggtgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgtttag aattggttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccata a                                     1341

```

&lt;210&gt; 49

&lt;211&gt; 1938

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes for full length ORF0657n containing SEQ ID  
 NO: 17 modified to contain a glycine afer the  
 amino terminus methionine and is codon optimized  
 for yeast expression

&lt;400&gt; 49

```

atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
gggtgtgctt ctgtcgctat ctccaccttg ttgttggtga tgtctaacgg tgaaggtcaa 120
gctgctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttgggt 180
tccccaacca ctaccactga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 240
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 300
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 360
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 420
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 480
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagtatt tttcaccgac 540
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 600
tacgaagggtg acaagaagtt gccaatlaag ttggtttcct acgacaccgt caaggactac 660
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 720
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 780
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttgggt 840
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 900
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 960
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 1020
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 1080
tccatgatgg acaccttcgt taagcaccca attaagactg gtatggtgaa cggtaagaag 1140
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1200
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1260
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1320
gacgggtcaat accacgtttag aattggttgac aaggaagctt tcaccaaggc taacaccgac 1380
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1440
ccatctaagc caaccccata tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1500
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1560
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1620
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1680
actaccaagg acgttggtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1740
ttgcaaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1800
aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1860
atgaccttgc cattgatggc tttgttgggt ttgtcttcca tcgttgcttt cgtcttgcca 1920
agaaagagaa agaactaa                                     1938

```

&lt;210&gt; 50

&lt;211&gt; 1710

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 20, is codon optimized for yeast expression, and encodes a methionine initiation codon

&lt;400&gt; 50

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttaa tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataa ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgtagg aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa

```

1710

&lt;210&gt; 51

&lt;211&gt; 1446

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 20 I+ region, is codon optimized for yeast expression, and encodes a methionine initiation codon

&lt;400&gt; 51

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240

```



```

acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact cgcgtccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatatag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatggtgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattggtgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagtaa 1446

```

<210> 52

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes the SEQ ID NO: 20 I region, is codon optimized for yeast expression, and encodes a methionine initiation codon

<400> 52

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctaccttga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact cgcgtccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatatag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatggtgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattggtgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320

```

ccatctaagc caaccccata a

1341

&lt;210&gt; 53

&lt;211&gt; 1938

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes for full length ORF0657n containing SEQ ID  
 NO: 20 modified to contain a glycine after the  
 amino terminus methionine and is codon optimized  
 for yeast expression

&lt;400&gt; 53

```

atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
ggtgttgctt ctgtcgctat ctccaccttg ttgttggtga tgtctaacgg tgaagctcaa 120
gctgctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 180
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 240
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 300
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 360
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 420
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggg 480
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 540
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 600
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 660
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 720
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 780
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 840
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 900
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 960
ttggacgaac aagtcaagtc cgtatcacc gaattccaaa acgttcaacc aactaacgaa 1020
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 1080
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1140
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1200
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1260
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1320
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1380
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1440
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1500
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1560
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1620
ccaaccaagg ttgtctccac tacccaaac gtcgctaagc caactaccgc ttcttccaag 1680
actaccaagg acgttggtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1740
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca ccaatccca aaacaacaag 1800
aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1860
atgaccttgc cattgatggc tttgttggtt ttgtcttcca tcggttgctt cgtcttgcca 1920
agaaagagaa agaactaa

```

1938

&lt;210&gt; 54

&lt;211&gt; 565

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH



&lt;400&gt; 54

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35				40					45				
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr
	50					55					60				
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile
65					70					75					80
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp
				85					90				95		
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys
			100					105					110		
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys
		115					120					125			
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly
	130					135					140				
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp
145					150					155					160
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr
				165					170				175		
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile
			180					185					190		
Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr
		195					200					205			
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys
	210					215					220				
Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys
225					230					235					240
Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp
				245					250				255		
Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp
			260					265					270		
Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe
		275					280					285			
Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr
	290					295					300				
Lys	Tyr	Ala	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp
305					310					315					320
Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys
				325					330				335		
Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met
			340					345					350		
Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn
		355					360					365			
Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp
	370					375					380				
Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr
385					390					395					400
His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp
				405					410					415	

Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr  
 500 505 510  
 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser  
 515 520 525  
 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn  
 530 535 540  
 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu  
 545 550 555 560  
 Asn Lys Ala Lys Ser  
 565

<210> 55

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 55

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Gly Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190

```

Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
    195                200                205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
    210                215                220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
225                230                235                240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
    245                250                255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
    260                265                270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Pro Ala Ile
    275                280                285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
    290                295                300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305                310                315                320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
    325                330                335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
    340                345                350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
    355                360                365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
    370                375                380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                390                395                400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
    405                410                415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
    420                425                430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
    435                440                445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
    450                455                460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                470                475                480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
    485                490                495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
    500                505                510
Pro Ile Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
    515                520                525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
    530                535                540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                550                555                560
Thr Gln Glu Asn Lys Ala Lys Ser
    565

```

&lt;210&gt; 56

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 56

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35					40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
65				70					75						80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Glu
			85					90					95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100					105					110		
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
		115				120						125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135						140			
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145				150					155						160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
			165					170					175		
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Ile	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195				200						205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225				230					235						240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
			245					250						255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275				280						285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
			325					330					335		
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355				360						365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385				390						395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
			405					410						415	

```

Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
      420      425      430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
      435      440      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
      450      455      460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465      470      475      480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
      485      490      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Val Lys
      500      505      510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
      515      520      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
      530      535      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545      550      555      560
Thr Gln Glu Asn Lys Ala Lys Ser
      565

```

```

<210> 57
<211> 568
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> ORF0657nH

```

```

<221> SITE
<222> 247
<223> Unknown

```

```

<400> 57
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
      20      25      30
Pro Val Ala Asn Ala Val Pro Val Ser Asn Lys Glu Val Glu Ala Pro
      35      40      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
      50      55      60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
      65      70      75      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Thr Lys Asn Pro Glu
      85      90      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Thr Asp Phe
      100      105      110
Glu Met Lys Lys Asn Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
      115      120      125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
      130      135      140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145      150      155      160

```

Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Ile	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Xaa	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
			405						410					415	
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val
		435					440					445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455					460				
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465					470					475					480
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser
				485					490					495	
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys
			500					505					510		
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser
		515					520						525		
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn
	530					535					540				
Leu	Leu	Lys	Thr	His	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Ile	Lys	Asn
545					550					555					560
Thr	Lys	Lys	Asp	Lys	Ala	Lys	Ser								
				565											

&lt;210&gt; 58

&lt;211&gt; 568



&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 58

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	1	5	10	15
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys	20	25	30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	35	40	45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	50	55	60	
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr	65	70	75	80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	85	90	95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	100	105	110	
Glu	Met	Lys	Lys	Glu	Asn	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	115	120	125	
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	130	135	140	
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	145	150	155	160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	165	170	175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	180	185	190	
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	195	200	205	
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	210	215	220	
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	225	230	235	240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	245	250	255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	260	265	270	
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	275	280	285	
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	290	295	300	
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	305	310	315	320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	325	330	335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Asn	Asp	Asp	Tyr	Trp	Lys		340	345	350	
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	355	360	365	
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	370	375	380	

```

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                      390                      395                      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                      405                      410                      415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                      420                      425                      430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                      435                      440                      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                      450                      455                      460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                      470                      475                      480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
                      485                      490                      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                      500                      505                      510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                      515                      520                      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
530                      535                      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                      550                      555                      560
Thr Gln Glu Asn Lys Ala Lys Ser
                      565

```

&lt;210&gt; 59

&lt;211&gt; 567

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 59

```

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1                      5                      10                      15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
                      20                      25                      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
                      35                      40                      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50                      55                      60
Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65                      70                      75                      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
                      85                      90                      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
                      100                      105                      110
Glu Met Asn Lys Lys Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser
115                      120                      125
Ser Ala Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130                      135                      140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145                      150                      155                      160

```

Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Asp  
 195 200 205  
 Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys  
 210 215 220  
 Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr  
 225 230 235 240  
 Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile  
 245 250 255  
 Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu  
 260 265 270  
 Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr  
 275 280 285  
 Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln  
 290 295 300  
 Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met  
 305 310 315 320  
 Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly  
 325 330 335  
 Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp  
 340 345 350  
 Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys  
 355 360 365  
 Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu  
 370 375 380  
 Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly  
 385 390 395 400  
 Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn  
 405 410 415  
 Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys  
 420 425 430  
 Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu  
 435 440 445  
 Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu  
 450 455 460  
 Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp  
 465 470 475 480  
 Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser Ser  
 485 490 495  
 Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro  
 500 505 510  
 Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala  
 515 520 525  
 Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile  
 530 535 540  
 Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr  
 545 550 555 560  
 Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 60

&lt;211&gt; 576

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 60

Ala	Glu	Glu	Thr	Gly	Val	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala
			20						25				30		
Lys	Pro	Val	Ala	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys
		35					40					45			
Glu	Val	Val	Ala	Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys
	50					55					60				
Ala	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro
65					70					75					80
Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu
			85						90					95	
Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala
			100					105					110		
Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr
		115					120						125		
Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile
	130					135						140			
Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln
145					150					155					160
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile
			165						170					175	
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe
		180						185					190		
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His
		195					200						205		
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala
210						215						220			
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr
225					230					235					240
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu
			245						250					255	
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys
		260						265						270	
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu
		275					280						285		
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro
290						295					300				
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Ala	Tyr
305					310					315					320
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His
			325						330					335	
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu
		340						345					350		
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
		355					360					365			
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile
370						375						380			

```

Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val
385                      390                      395                      400
His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val
                      405                      410                      415
Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys
                      420                      425                      430
Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro
                      435                      440                      445
Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp
                      450                      455                      460
Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn
465                      470                      475                      480
Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro
                      485                      490                      495
Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val
                      500                      505                      510
Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr
                      515                      520                      525
Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
530                      535                      540
Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
545                      550                      555                      560
Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
                      565                      570                      575

```

&lt;210&gt; 61

&lt;211&gt; 572

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 61

```

Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1                      5                      10                      15
Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
                      20                      25                      30
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala
                      35                      40                      45
Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Val Lys Glu
50                      55                      60
Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro Ala Ala Lys Ala
65                      70                      75                      80
Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile
                      85                      90                      95
Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg
                      100                      105                      110
Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr
                      115                      120                      125
His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser
130                      135                      140
Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys
145                      150                      155                      160

```



Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser  
 165 170 175  
 Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn  
 180 185 190  
 Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys  
 195 200 205  
 Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr  
 210 215 220  
 Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys  
 225 230 235 240  
 Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr  
 245 250 255  
 Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu  
 260 265 270  
 Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val  
 275 280 285  
 Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys  
 290 295 300  
 Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu  
 305 310 315 320  
 Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr  
 325 330 335  
 Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp  
 340 345 350  
 Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile  
 355 360 365  
 Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Cys Val  
 370 375 380  
 Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr  
 385 390 395 400  
 Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala  
 405 410 415  
 Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys Glu Gln Gln Asp  
 420 425 430  
 Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro Ser Lys Pro Thr  
 435 440 445  
 Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp  
 450 455 460  
 Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser  
 465 470 475 480  
 Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro Ala Lys Ala Glu  
 485 490 495  
 Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln  
 500 505 510  
 Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr Thr Lys Asp Val  
 515 520 525  
 Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu  
 530 535 540  
 Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln  
 545 550 555 560  
 Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570

&lt;210&gt; 62

&lt;211&gt; 572

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 62

Ala	Glu	Glu	Thr	Gly	Val	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	1	5	10	15
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	20	25	30	
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Val	Ala	35	40	45	
Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Val	Lys	Glu	50	55	60	
Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro	Ala	Ala	Lys	Ala	65	70	75	80
Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	85	90	95	
Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	100	105	110	
Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	115	120	125	
His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	130	135	140	
Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	145	150	155	160
Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	165	170	175	
Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	180	185	190	
Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	195	200	205	
Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	210	215	220	
Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	225	230	235	240
Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	245	250	255	
Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	260	265	270	
Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	275	280	285	
Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	290	295	300	
Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	305	310	315	320
Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	325	330	335	
Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	340	345	350	
Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	355	360	365	
Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	370	375	380	

Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr  
 385 390 395 400  
 Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala  
 405 410 415  
 Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys Glu Gln Gln Asp  
 420 425 430  
 Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro Ser Lys Pro Thr  
 435 440 445  
 Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp  
 450 455 460  
 Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser  
 465 470 475 480  
 Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro Ala Lys Ala Glu  
 485 490 495  
 Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln  
 500 505 510  
 Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr Thr Lys Asp Val  
 515 520 525  
 Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu  
 530 535 540  
 Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln  
 545 550 555 560  
 Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570

<210> 63  
 <211> 566  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 63  
 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala  
 20 25 30  
 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala  
 35 40 45  
 Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu  
 50 55 60  
 Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro  
 65 70 75 80  
 Ile Leu Asn Lys Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys  
 85 90 95  
 Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met  
 100 105 110  
 Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val  
 115 120 125  
 Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu  
 130 135 140  
 Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly  
 145 150 155 160

Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp  
 165 170 175  
 Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys  
 180 185 190  
 Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr  
 195 200 205  
 Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe  
 210 215 220  
 Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys  
 225 230 235 240  
 Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln  
 245 250 255  
 Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu  
 260 265 270  
 Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu  
 275 280 285  
 Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp  
 290 295 300  
 Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met  
 305 310 315 320  
 Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys  
 325 330 335  
 Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe  
 340 345 350  
 Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn  
 355 360 365  
 Asn Thr Arg Thr Ile Ile Phe Pro Tyr Ile Glu Gly Lys Thr Leu Tyr  
 370 375 380  
 Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln  
 385 390 395 400  
 Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala  
 405 410 415  
 Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu  
 420 425 430  
 Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Pro Pro Val Glu Lys  
 435 440 445  
 Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Thr Gln Ser Pro  
 450 455 460  
 Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys  
 465 470 475 480  
 Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr  
 485 490 495  
 Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr  
 500 505 510  
 Thr Ala Ser Ser Glu Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly  
 515 520 525  
 Pro Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys  
 530 535 540  
 Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln  
 545 550 555 560  
 Glu Asp Lys Ala Lys Ser  
 565

&lt;210&gt; 64

&lt;211&gt; 8

<212> PRT  
<213> Artificial Sequence

<220>  
<223> His-Tag

<400> 64  
Leu Glu His His His His His His  
1 5

<210> 65  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 65  
ctggccgctcg ttttac 16

<210> 66  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 66  
caggaaacag ctatgac 17

<210> 67  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 67  
aaccggtttt ccatggggaa caaacagcaa aaagaattt 39

<210> 68  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 68  
accggtttct cgaggttttt acgttttcta ggtaatac 38

<210> 69



<211> 109  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 69  
atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60  
ggtgttgctt ctgtcgctat ctccaccttg ttgttggtga tgtctaacg 109

<210> 70  
<211> 110  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 70  
gttggggaag cgacagcttc ggtctttggt tgagcttcag tgttggtacc accagtttct 60  
tcagcagcag cttgagcttc accgtagac atcaacaaca acaagggtgga 110

<210> 71  
<211> 110  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 71  
agaccgaagc tgtcgcttcc ccaaccacta cctctgaaaa ggctccagaa actaagccag 60  
ttgctaacgc tgtctccggt tctaacaagg aagtcgaagc tccaacctcc 110

<210> 72  
<211> 109  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 72  
tggtagcctt agcagctggc ttgacttcct tagtttctct tggagccttg acttccttaa 60  
cttccttagc ttccttagtt tcggagggtg gagcttcgac ttccttggt 109

<210> 73  
<211> 108  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

&lt;400&gt; 73

aagtcaagcc agctgctaag gctaccaaca acacttaccc aattttgaac caagaattga 60  
gagaagctat taagaaccca gctatcaagg acaaggacca ctccgctc 108

&lt;210&gt; 74

&lt;211&gt; 109

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 74

tggcttgaca gaggacgcgt agtggtagaa ttgttgggta ccgtccttct tcttcatttc 60  
gaagtcgatt ggtctagagt ttggagcgga gtggtccttg tccttgata 109

&lt;210&gt; 75

&lt;211&gt; 102

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 75

accactacgc gtcctctgtc aagccagcta gagttatttt caccgactct aagccagaaa 60  
tcgaattggg tttgcaatcc ggtcaattct ggagaaagtt cg 102

&lt;210&gt; 76

&lt;211&gt; 104

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 76

ctgatgtaag cgtagtcctt gacgggtgtcg taggaaacca acttaattgg caacttcttg 60  
tcaccttcgt agacttcgaa ctttctccag aattgaccgg attg 104

&lt;210&gt; 77

&lt;211&gt; 109

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 77

caccgtcaag gactacgctt acatcagatt ctccgtttct aacggtacta aggctgtcaa 60  
gattgtctct tccaccact tcaacaacaa ggaagaaaag tacgactac 109

&lt;210&gt; 78

&lt;211&gt; 109

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 78

aacttttcag ccttgtagtc ttcttcggtc ttgaacttgt cagcagagtt gtaaattggg 60  
tgagcgaatt ccatcaaagt gtagtcgtac ttttcttcct tgttgttga 109

<210> 79

<211> 106

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 79

ccgaagaaga ctacaaggct gaaaagttgt tggctccata caagaaggct aagactttgg 60  
aaagacaagt ttacgaattg aacaagatcc aagacaagtt gccaga 106

<210> 80

<211> 109

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 80

tcggtgatag cggacttgac ttgttcgtcc aaagccttct tgggtgtcttc caacttcttc 60  
ttgtattcag ccttcaactt ttctggcaac ttgtcttgga tcttgttca 109

<210> 81

<211> 109

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 81

cgaacaagtc aagtcgcta tcaccgaatt ccaaaacggt caaccaacta acgaaaagat 60  
gactgacttg caagacacta agtacgtcgt ctacgaatcc gtcgaaaac 109

<210> 82

<211> 109

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 82

tttccatgac catgtacttc ttaccgttca acataccagt cttaattggg tgcttaacga 60

aggtgtccat catggattcg ttgttttcga cggattcgta gacgacgta

109

<210> 83

<211> 109

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 83

gaacggtaag aagtacatgg tcatggaaac cactaacgac gactactgga aggacttcat 60  
ggttgaaggt caaagagtca gaaccatctc caaggacgct aagaacaac 109

<210> 84

<211> 101

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 84

gtcttgacgt gaaccttgac gatagcgctg tacaaagtct taccttcaac gtatgggaag 60  
ataatgggttc tagtggttgtt cttagcgctcc ttggagatgg t 101

<210> 85

<211> 106

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 85

cgctatcgtc aaggttcacg tcaagactat tgactacgac ggtcaatacc acgttagaat 60  
tgttgacaag gaagctttca ccaaggctaa caccgacaag tccaac 106

<210> 86

<211> 96

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 86

tgggggttggc ttagatgggg tagctgggggt agcttccttc ttagcagagt tgtcttggtg 60  
ttccttcttg ttggacttgt cggtgtagc cttggt 96

<210> 87

<211> 85

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 87

cagctacccc atctaagcca accccatctc cagttgaaaa ggaatctcaa aagcaagact 60  
cccaaaagga cgacaacaag caatt 85

<210> 88

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 88

gttggcttgg tagctggagt cttgtcctta ccggattcag aagacgcgtc gttttccttt 60  
tcgacggatg gcaattgctt gttgtcgtcc ttttgggagt 100

<210> 89

<211> 101

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 89

ggacaagact ccagctacca agccaactaa gggatgaagtt gaatcttcct ctactactcc 60  
aaccaagggt gtctccacta ccaaaaacgt cgctaagcca a 101

<210> 90

<211> 101

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 90

agcagagtcc ttagcttcag aggaaccagc agaagtttgg acaacgtcct tggtagtctt 60  
ggaagaagcg gtagttggct tagcgacgtt ttgggtagtg g 101

<210> 91

<211> 91

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 91

ggttcctctg aagctaagga ctctgctcca ttgcaaaagg ctaacatcaa gaacaccaac 60  
gacggtcaca cccaatccca aaacaacaag a 91



<210> 92  
<211> 98  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 92  
gtgaagaatc caacaaggac atgaccttgc cattgatggc tttgttggct ttgtcttcca 60  
tcgttgcttt cgtcttgcca agaaagagaa agaactaa 98

<210> 93  
<211> 98  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 93  
gtgaagaatc caacaaggac atgaccttgc cattgatggc tttgttggct ttgtcttcca 60  
tcgttgcttt cgtcttgcca agaaagagaa agaactaa 98

<210> 94  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 94  
cttaaagctt atgtcacttt ctcttgtatc g 31

<210> 95  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 95  
tgataagctt gctcaatggc tctcttcctc 30

<210> 96  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 96

aaccggtttg gatccacaa aacaaaatgg gtaacaagca aaaaaggaa ttc 53

<210> 97

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 97

aaccggtttg gatccttagt tctttctctt tcttggaag ac 42

<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 98

gctgaagaaa ctggtggtac caac 24

<210> 99

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 99

gtcacggatc ctttaagactt agccttggtt tcttgagtgt tc 42

<210> 100

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 100

gggggggatcc cacaaaacaa aatgggtgaa gaaactgggtg g 41

<210> 101

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 101  
gggggggggat ccttaagact tagccttggt ttcttgagt

39

<210> 102  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 102  
gggggggatcc cacaaaacaa aatggctgaa gaaactggtg g

41

<210> 103  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 103  
gggggggggatc cttagttctt tctctttctt gg

32

<210> 104  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 104  
ctccggatcc cacaaaacaa aatggctgaa gaaactggt

39

<210> 105  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 105  
gctgccggga tccttatggg gttggcttag atggggta

38

<210> 106  
<211> 644  
<212> PRT  
<213> S. aureus

&lt;400&gt; 106

Met	Asn	Lys	Gln	Gln	Lys	Glu	Phe	Lys	Ser	Phe	Tyr	Ser	Ile	Arg	Lys
1				5					10					15	
Ser	Ser	Leu	Gly	Val	Ala	Ser	Val	Ala	Ile	Ser	Thr	Leu	Leu	Leu	Leu
		20						25					30		
Met	Ser	Asn	Gly	Glu	Ala	Gln	Ala	Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn
		35					40					45			
Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	Ala	Leu	Ala	Ser	Pro	Thr	Thr	Thr
	50					55					60				
Thr	Glu	Lys	Ala	Pro	Glu	Thr	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val
65					70					75					80
Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys
				85					90					95	
Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro
			100					105					110		
Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu
		115					120					125			
Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala
	130					135					140				
Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu
145					150					155					160
Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile
				165					170					175	
Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln
			180					185					190		
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile
		195					200					205			
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe
	210					215					220				
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His
225					230					235					240
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala
				245					250					255	
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr
			260					265					270		
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu
		275				280						285			
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys
	290					295					300				
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu
305					310					315					320
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro
				325					330					335	
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr
			340					345					350		
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His
		355				360						365			
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu
	370					375					380				
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
385					390					395					400
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Ile	Asn	Asn	Thr	Arg	Thr	Ile	Ile
				405					410					415	
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val
			420					425					430		

His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 435 440 445  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys  
 450 455 460  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro  
 465 470 475 480  
 Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 485 490 495  
 Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu Asn  
 500 505 510  
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro  
 515 520 525  
 Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val  
 530 535 540  
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys Thr  
 545 550 555 560  
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp  
 565 570 575  
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His  
 580 585 590  
 Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 595 600 605  
 Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro Leu  
 610 615 620  
 Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro Arg  
 625 630 635 640  
 Lys Arg Lys Asn

&lt;210&gt; 107

&lt;211&gt; 644

&lt;212&gt; PRT

&lt;213&gt; S. aureus

&lt;400&gt; 107

Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys  
 1 5 10 15  
 Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu  
 20 25 30  
 Met Ser Asn Gly Glu Ala Gln Ala Glu Glu Thr Gly Gly Thr Asn  
 35 40 45  
 Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr  
 50 55 60  
 Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser Val  
 65 70 75 80  
 Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys  
 85 90 95  
 Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro  
 100 105 110  
 Ala Thr Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu  
 115 120 125  
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala  
 130 135 140  
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Glu Asn Gly Glu  
 145 150 155 160



Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile
				165					170					175	
Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln
			180					185					190		
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile
		195					200					205			
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe
	210					215					220				
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His
225					230					235					240
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala
			245						250					255	
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr
			260					265						270	
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu
	275						280					285			
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys
	290					295					300				
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu
305					310					315					320
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro
			325						330					335	
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr
		340						345					350		
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His
	355						360					365			
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu
	370					375					380				
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
385					390					395					400
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile
			405						410					415	
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val
			420					425					430		
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val
	435						440					445			
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys
	450					455				460					
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro
465					470					475					480
Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp
			485					490						495	
Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn
			500					505					510		
Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro
	515						520					525			
Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val
	530					535					540				
Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr
545					550					555					560
Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp
			565						570					575	
Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His
			580					585					590		

Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser
		595					600					605			
Leu	Pro	Gln	Thr	Gly	Glu	Glu	Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro	Leu
	610					615					620				
Met	Ala	Leu	Leu	Ala	Leu	Ser	Ser	Ile	Val	Ala	Phe	Val	Leu	Pro	Arg
625					630					635					640
Lys	Arg	Lys	Asn												